

What Is Claimed Is:

1. A method in a computer system for analyzing and displaying data on gene expression in a molecular topography, comprising:

(a) generating a gene expression profile of a plurality of gene-expression indicating polynucleotides including for each of the polynucleotides:

(i) a first value for a first polynucleotide characteristic,

(ii) a second value for a second polynucleotide characteristic different from said first characteristic, and

(iii) a third value that is a measure of the quantity of the polynucleotide;

(b) calculating for each polynucleotide from the first, second and third values, a position and a peak in a multi-dimensional display space; and

(c) displaying the peak for each polynucleotide at the position for the polynucleotide in the display; the resulting display representing thereby a molecular topography of gene expression.

2. A method in a computer system for analyzing and displaying data on gene expression in a molecular topography according to claim 1, further comprising:

(d) generating a file containing information for display relating to a peak in the molecular topology, and

(e) linking the information for display to the related peak in the molecular topography.

3. The method of claim 1, wherein: i) the first characteristic is a sequence identifier, and ii) the second characteristic is a measure of size.

4. The method of claim 1, wherein values of the first and second characteristics are arranged along first and second ordinates that define a plane, the values of the first and second characteristics for each polynucleotide define a position in the plane, and the peak calculated for each polynucleotide is displayed at the defined position for that polynucleotide in the plane.

5. The method of claim 1, wherein the polynucleotides are cDNAs or fragments thereof.

6. The method of claim 5, wherein the polynucleotides are 3'-end fragments of restriction enzyme cleaved cDNAs.

7. The method of claim 6, wherein the first characteristic is a sequence identifier, and the second characteristic is a measure of size.

8. The method of claim 7, wherein the sequence identifier is the combination of an anchor sequence of a cDNA synthesis primer and a restriction enzyme cleavage reaction specificity.

9. The method of claim 8, wherein values of the first and second characteristics are arranged, respectively, along first and second ordinates, the first and second ordinates defining a plane, the values of the first and second characteristics for each polynucleotide by their location on the first and second ordinates define a position in the plane, and the peak for each polynucleotide is displayed at the position of the polynucleotide on the plane.

10. The method of claim 9, wherein the 3'-end fragments are generated by READS.

11. A method in a computer system for displaying differences in gene expression, comprising:

(1) for each of two gene expression profiles to be compared generating a molecular topography according to claim 1,

(2) for each position in the two co-ordinate space subtracting the measure of quantity in the first profile from the measure of quantity in the second profile;

(3) for each position, generating a peak for display from the difference; and

(4) displaying the respective difference peak at each of the positions in the two co-ordinate space.

12. The method of claim 11, wherein differences are displayed only if they meet or exceed a threshold value.

13. A method in a computer system for comparing gene expression, comprising:

(1) for each of two gene profiles to be compared generating a molecular topography according to claim 1,

(2) for each position in the two co-ordinate space subtracting a first measure of quantity in the first profile from a second measure of quantity in the second profile to generate respective difference values;

(3) calculating from the respective difference values a measure of difference of the two profiles.

14. The method of claim 13, wherein the first profile is a standard reference profile and the second profile is a the profile of a test sample.

15. The method of claim 14, wherein comparison of the test sample profile with the standard reference profile is diagnostic of a condition or disease.

16. The method of claim 15, wherein the first profile is a profile of a reference sample and the second profile is a profile of a test sample.

17. The method of claim 16, wherein comparison of the profile of the test sample with the profile of the reference sample is diagnostic of a condition or disease.

18. The method of claim 13 wherein the difference value is set to zero when the difference between the first measure and the second measure is less than two-fold.

19. The method of claim 13 wherein the first profile is identical to the second profile when all the respective first and second measures are identical.

20. The method of claim 13 wherein the first profile is similar to the second profile when the average difference between the respective first and second measures is less than a predefined amount.

21. The method of claim 20 wherein the differences are weighted based on a relative magnitude of the difference.

22. A method in a computer system for displaying a series of in gene expression profiles in a molecular movie, comprising:

1. generating a plurality of molecular topographies according to claim 1, and

(2) displaying the molecular topographies in succession.

23. The molecular movie of claim 23, wherein the molecular topographies are delta plots.